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Evaluation of Combining Ability and Heterosis for Achene Yield and Related Traits in Sunflower (Helianthus Annuus l.) Through Line x Tester Analysis

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Abstract

Four sunflower lines, eight testers, and 32 crosses developed in line × tester fashion were evaluated for Specific Combining Ability (SCA) effects in two replications randomized complete block design, in Nimpith, during 2015-2016. Genetic variability among genotypes was assessed for days to flowering, plant height, head diameter, percentage of filled achenes, 100 achene weight, hull content, volume weight, achene yield kg/hectare, oil content and oil yield kg/hectare. Crosses CMS-302A × EC-623011, CMS-302A × R-12-96, CMS-16A × EC-602060, P-2-7-1A × EC-601958, CMS-850A × EC-623029, CMS-850A × EC-512682 and CMS-16A × R-341 had significant and positive SCA effects for achene yield kg/hectare. Seven best SCA crosses are recommended to be the best hybrids for cultivation. Non-additive type of gene action was found for all of the plant traits, which is desirable for heterosis breeding and may be exploited in hybrid seed production.

Keywords: Circadian rhythms; Pathophysiology; Rhythm-regulation; Melatonin; Metabolite 6-Sulfatoxymelatonin; Bipolar problem; Organic rhythms

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Introduction

Sunflower (*Helianthus annuus L.*) is grown in different parts of the world as an important source of vegetable oil and protein. It is the fourth important oilseed crop after soybean, groundnut and mustard. Sunflower is native to North America and has spread across the globe owing to its wider adaptability and short growing season. Sunflower is a rich source of high quality edible oil (35%-43%) owing to high degree of polyunsaturated fatty acid (50% -60% linoleic acid). Its oil is considered to have a premium quality due to its light colour, mild flavor and ability to withstand high cooking temperatures and also has anti-cholesterol properties. Sunflower being a photo-thermo insensitive crop can be grown year around viz. during *rabi/kharif* or spring season. In India it is mainly grown in Karnataka, Maharashtra, Andhra Pradesh and Tamil Nadu. However, now it has spread to North Indian states i.e. Punjab, Haryana, Uttar Pradesh and Bihar, mainly as a spring season crop. Due to increasing demand for edible oils, there is a need to develop new sunflower hybrids suited to different agro-climatic zones of India with improved seed yield and oil content. Sunflower hybrid cultivars are more uniform and higher-yielding than open pollinated varieties [1]. Single cross hybrids of sunflower are preferred by farmers due to their high yield performance, quality and uniformity. Some researchers, for example, Raposo et al. (2004), Kaya (2005) and Darvishzadeh et al. (2010a) believed that the larger genetic distance between two parental lines resulted in generation of high performing hybrids [2-4]. Information on genetic distance and combining abilities among parents i.e. A and R lines is prerequisite in hybrid development programs. Genetic diversity is considered to be an important tool for realizing heterotic response in F1 and a broad spectrum of variability in the segregating generations. Kempthorne (1957) developed several biometrical techniques to generate information on gene action and mode of inheritance of various characters, among which line × tester analysis has been widely used for genetic analysis in large number of crop plants [5].

Material and Methode

The crossing programme was undertaken during *rabi* 2015-2016 by adopting line × tester mating design consisted 4 lines (CMS-302A, CMS-16A, P-2-7-1A and CMS-850A) and 8 testers (EC-601978, EC-623029, R-341, EC-602060, R-12-96, EC-601958, EC-623011 and EC-512682) and generated thirty two hybrids at Sunflower AICRP centreNimpith, West Bengal. The resultant 32 hybrids along with their 12 parents and three checks viz., DRSH-1, LSFH-171 and KBSH-53 were evaluated in randomized block design with two replications at Ramkrishna Ashram KVK, South 24-Parganas (Sundarbans) West Bengal, India during *rabi* 2016-2017. The germinated seed of sunflower used and one seedling per hill was maintained throughout the cropping period. Plot size was three rows of three meter length. The soil texture is clay loam. Three irrigations were provided during the cropping period. One foliar spray was given with Boron (@2 g/lit. of water at ray floret opening stage for good seed setting. Row to row spacing was 60 cm and plant to plant spacing was 30 cm. Recommended packages and practices were adopted to raise a healthy crop. Necessary prophylactic measures were taken up to safeguard the crop from pests and diseases. The data was recorded on ten randomly selected plants from each plot on days to 50% flowering, days to maturity, plant height at harvest (cm), head diameter per plant (cm), seed weight per head (g), 100-seed weight (g), hull content (%), volume weight (g/100 ml). The seed yield (kg/ha) and oil yield (kg/ha) were estimated on plot basis. Oil content in the seeds of each entry was determined through non-destructive method by utilizing Nuclear Magnetic Resonance (NMR) technique at ICAR-Indian Institute of Oilseeds Research, Rajendra nagar, Hyderabad. The combining ability effects were estimated as per procedure suggested by Kempthorne (1957) [5]. Heterosis, heterobeltiosis and economic heterosis has been estimated as per the methods suggested by Fonesca and Patterson (1968) [6].

Result and Discussion

The analysis of variance revealed that the genotypes exhibited highly significant themselves. The parents exhibited significant differences for all the traits studied except filled seed per plant, whereas crosses, parents vs crosses exhibited significant differences for all the traits studied (**Table 1**). The mean sum of squares due to crosses was split into lines, testers and interactions (line × tester) effects, the effects of lines and testers were significant for all the characters. The interaction effects (lines × testers) were found to be significant for all the characters studied **(Table 1**). However, line × tester interaction was significant for all characters except oil yield. Significant difference within various components indicated the presence of genetic variability in the breeding material used in the study. This genetic variability may be exploited in the breeding programs for improvement of sunflower achene yield and its related traits. Significant differences have also been reported by early researchers among sunflower genotypes (Gvozdenovic et al., 2005; Habib et al., 2007), males and females parents (Jayalakshmi et al., 2000; Kannababu and Karivaratharaju, 2000; Monotti et al., 2000; Sharma et al., 2003) and L × T interaction (Laureti and Del Gatto, 2001; Ortiset al., 2005; Binodh et al., 2008) for achene yield and its components [7-15]. The variance component due to Specific Combining Ability (SCA) was higher in amount than that of general combining ability (**Table 1**) for all the characters demonstrating prevalence of non-additive (dominant, over dominance and epistasis) type of gene action, and therefore, heterosis breeding may be rewarded which is in agreement with the findings of Shankar et al. (2007) [16]. Dominant gene effects were reported for days to flowering, number of leaves per plant, head diameter by Skoric et al. (2000) and Marinkovic et al. (2000) [17-18]. Over dominance effects for plant height, leaf area and 100-achene weight were also reported by Skoric et al. (2000) [17]. The mean performance of parents (corresponding B lines of CMS lines and testers), hybrids and standard checks for twelve quantitative traits studied are presented in **Table (2-4**). Heterosis was estimated for seed yield and yield components in 32 hybrids was expressed as increase or decrease over mid parent value (heterosis). The results are presented in **Table (2-4**). With the point of view of objectives of the present study selection criteria for identification of suitable hybrids with the parameters like; days to flowering for early maturity, plant height, heat diameter, percent filled achenes, 100-achene weight and achene yield kg/hectare for economic yield must be under consideration. In sunflower, positive SCA effects are desirable for all the traits studied except for days to 50% flowering, plant height and hull content for which negative SCA effects are desirable. Cross combinations (**Table 5**); CMS-16A x R-341 depicted excellent SCA performance for almost all the characters under study, while CMS-302A × EC-623029, CMS-16A × EC-623029 and P-2-7-1A × R-341 revealed highly significant SCA effects for more than 80% traits, respectively. Hybrids P-2-7-1A × EC-623011, CMS-850A × EC-623011, CMS-302A × EC-512682, P-2-7-1A × R-341, CMS-302A × EC-602060, CMS-16A × EC-601978, CMS-16A × EC-623029 and CMS-850A × R-12-96 illustrated high negatively significant SCA effects for days to flowering. This character might be due to low × low, high × low and low × high combining parents indicating non-additive gene action so, heterosis breeding may be rewarded. These results were in conformity with the earlier findings of Goksoy and Turan (2005), Gvozdenovicet al. (2005), Ortiset al. (2005), Hladniet al. (2006) [7, 14, 19-20]. Hybrid progeny; CMS-302A × EC-623011, CMS-302A × R-12-96, CMS-16A × EC-602060, P-2-7-1A × EC-601958, CMS-850A × EC-623029, CMS-850A × EC-512682 and CMS-16A × R-341 demonstrated highly significant SCA effects for seed yield kg/hectare. These results are in accordance with the findings of Sharma et al. (2003); Ortiset al. (2005); Hladniet al. (2006). Enchevaet al. (2015) observed standard heterosis in sunflowers for seed yield and oil yield [12, 14, 20-21]. For oil yield kg/hectare cross combinations; CMS-302A × EC-623011, P-2-7-1A × EC-601958, CMS-16A × EC-602060, CMS-850A × EC-512682, CMS-16A × R-341 and CMS-850A × EC-601978 demonstrated highly significant and positive SCA effects. Highest negative and significant SCA effects for hull content was demonstrated by hybrid CMS-302A × EC-623029 followed by P-2-7-1A x EC-602060, CMS-302A x EC-623011, P-2-7-1A x EC-512682 and CMS-850A x EC-601978.

The crosses with significant SCA effects in the desirable direction involved parents with high × high or high × low or low × low GCA effects, indicating high performance of these crosses due to additive, dominance and epistasis gene interaction. Asif et al. (2013) reported similar type of results. Based on SCA, promising hybrid combinations were identified for each trait (Table 5) [22].

Conclusion

According to above research study, it is concluded that breeding material evaluated has adequate genetic variability that may be exploited in further breeding programs. SCA and GCA ANOVAs proposed these characters under control of non-additive gene action. Further analysis revealed over-dominant gene action controlling these plant traits. Therefore, heterosis breeding is suggested for improvement in yield and related traits using this sunflower breeding material. Cross combinations; CMS-16A x R-341, CMS-302A × EC-623029, CMS-16A x EC-623029 and P-2-7-1A × R-341 depicted excellent SCA performance for more than 80% traits under study. Finally, it is concluded that non-additive type of gene action was found for all of the plant traits, which is desirable for heterosis breeding and may be exploited in hybrid seed production

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